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Title:
Perfect score:
Sequence:
                                                                                                                                                                                 Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Query
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1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      March 14, 2003, 09:23:29; Search time 20.8151 Seconds (without alignments) 3900.178 Million cell updates/sec
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sp_mhc:*
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Q64906 alcelaphine
Q9j5f6 fowlpox vir
Q9c0b8 homo sapien
Q8tb71 homo sapien
Q8tb71 homo sapien
Q8tdV7 homo sapien
Q8tdV7 homo sapien
Q9c0c4 homo sapien
Q9fx23 mus musculu
Q9hbr1 homo sapien
Q8fgu9 gallus gall
Q9ns98 homo sapien
Q9h2e6 homo sapien
Q9p2h9 homo sapien
Q9p2h9 homo sapien
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imilarity	rructure 1:6517- 1:6517- 0M N.A 7-199 MAY-199	ROM N.A. 10; 12:201573; pr Fleckens: ne herpes: rol. 76:11 ROM N.A. 14:04 14:04 15:11 PFlanz R	96 (TrEMBLrel. 0 96 (TrEMBLrel. 0 01 (TrEMBLrel. 0 0 GENBANK ACCESS ne herpesvirus 1 dSDNA viruses, n esvirinae; Rhadi D=35252;	PRELIMINAR		14.0 13.3 13.3 13.5 12.5 12.5 12.4 12.4 12.1 11.9 111.9 111.9 111.9 111.9 111.9 111.9 111.9 111.9 111.9 111.9 111.9 111.3 10.8 10.8 10.8 10.8 10.8 10.8 10.8 10.8
42.8	R., Fleck R., Fleck R., Fleck A4475.1; AC58054.1. 27; Sema. na; 1.	Pubmed=90 stein B svirus t 1063-106	rel. 01 rel. 01 rel. 17 ACCESSI irus 1 ses, no Rhadin	NARY;		418 761 1202 1202 1028 1028 1028 1028 1028 102
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Score 907 Pred. No.	ph jin	59; 1 has 95). 95).	11, Created) 11, Last seque 17, Last annot 1310N number L2 1510N stage; 100 RNA stage; 1100 RNA stage; 1100 RNA stage;	PRT;	ALIGNMENTS	096JU9 08WUA9 08P283 09P283 09P2494 09P707 09U707 09U707 09U798 09HAH9 09LYB 09HAH9 09LYB 09P4H0 09LYB 09P4H0 09LYB 09F5 09F5 09F5 09F5 09F5 09F5 09F5 09F5
.5; DB 12; 8.1e-71;	erpesvirus 1 g k/DDBJ databas 567E706E CRC64	semaphorin-like	<pre>puence update) cotation update) L26081. it herpesvirus). ;; Herpesviridae;</pre>	653 AA.	MENTS	
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Matches

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Conservative

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Mismatches

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Best Local
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Pfam; PF01437; PSI; I.
Pfam; PF01403; Sema; 1.
SMART; SM00423; PSI; 1.
SEQUENCE 612 AA; 69514
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

Afonso C.L., Tulman E.R., Lu Z., Zs
Submitted (OCT-1999) to the EMBL/Ge
EMBL; AF198100; AAF44391.1; -.

InterPro; IPR003659; Plexin-like.
InterPro; IPR002165; Plexin_repeat.
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MEDLINE-20193820; PubMed-10729156;
Afonso C.L., Tulman E.R., Lu Z., Z:

"The genome of fowlpox virus.";
J. Virol. 74:3815-3831(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2002 (TrEMBLrel. 21,
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VGGRGKVYHFNFPEGKNASV--RTVNIGSTKGSCQDKQDCGNYITLLERRGNGLLVCGTN 143
                                                              IGVTNTVYVVNTTDKSNITVDFSPDNVSTQSGA-----NYITFIGGYDDKILVCGTN 110
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    15, Last sequence update)
    1. 21, Last annotation updat vaccinia A39R homolog.

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EMBL/GenBank/DDBJ
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                                                                                                                                                   Score 504; DB 12;
Pred. No. 1.6e-35;
7; Mismatches 107;
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DDBJ databases
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Best Local :
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01-JUN-2001
01-JUN-2001
01-JUN-2002
KIAA1745 pro
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InterPro: IPR002165; Plexin_repeat.
InterPro: IPR001627; Sema.
Pfam; PF01437; PSI; 1.
Pfam; PF01403; Sema; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Homo sapiens (Human).
'harvota; Metazoa; Chordata; harvota; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nagase T., Kikuno R., Hattori A., Kondo Y., Okumura "Prediction of the coding sequences of unidentified The complete sequences of 100 new cDNA clones from b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for large proteins in vitro.";
DNA Res. 7:347-355(2000).
EMBL; AB051532; BAB21836.1; -.
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129; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                    PPPPGRAAPSAPRARVL-----WVAA 41
DPAISRSQSLRPTKTESSLNWLQDPAFVASAYIPESLGSLQGDDDKIYFFFSETGQEFEF
                                           IPRFRRIRGESELYTSDTV--MQNPQFIKATIVHQD----
                                                                                         SPMCTYINMENFTLARDEKGNVLLEDGKGRCPFDPNFKSTALVVDGELY-TGTVSSFQGN
                                                                                                                                      KPSCW--NLVNDSVV-
                                                                                                                                                                                    SNLSFLPGGEYQELLWGADAEKKQQCSFKGKDPQRDCQNYIKILLPLSGSHLFTCGTAAF
                                                                                                                                                                                                                 -----FPEGKNASVRTVNIGSTKGSCQDK-----QDCGNYI-TLLERRGNGLLVCGTNAR 145
                                                                                                                                                                                                                                                                               ------PRIS-LPLGSEERPFLRFEAEHISNYTALLLSRDGRTLYVGAREALFALS
                                                                                                                                                                                                                                                                                                                                                                        PPEPEPROTVAPALRMLRTAMGLRSWLAAPWGALPPRPPLLLLLLLLLLLQPPPPTWALS
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17,
21,
                                                                                                                                      -MSLGEMKGYAPFSPDENSLVLFEGDEVYSTIRKQEYNGK 197
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Pred. No. 6.6e-26;
4; Mismatches 167;
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                               -QAYDDKIYYFFREDNPDKNP
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Best Local S
Matches 127
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Submitted (PEB-2002) to the EMBL/GenBank/DDBJ databases EMBL; BC024220; AAH24220.1; -.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
Hypothetical 83.0 kDa protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein. SEQUENCE 748 AA; 8
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                                                                                                                                                   CVYSLGDIDRVF-
                                                                                                                                                                                                    NKWTTFLKARLVCSVPGVEGDTHFDQLQDVFLL--SSRDHRTPLLYAVFSTSSIFQGSAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GEMKGYAPFSPDENSLVLFEGDEVYSTIRKQEYNGKIPRFRRIRGESELYT---SDTVMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KDIGT-----ECMNFVKLLHAYNRTHLLACGTGAFHPTCAFVEVGHRAEEPVLRLDPGRI
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                                                FQVADSHPEVAQRVEPMG
                                                                                              {\tt CVYSMNDVRRAFLGPFAHKEGPMHQWVSYQGRVPYPRPGMC-PSKTFGTFSSTKDFPDDV}
                                                                                                                                                                                                                                                    SKWNTFLKAMLVCS--DAATNRNFNRLQDVFLLPDPSGQWRDTRVYGVFSNP--WNYSAV
                                                                                                                                                                                                                                                                                                       EPKFVKVFWIPESENPDDDKIYFFFRETAVEAAPALGRLSVSRVGQICRNDVGGQRSL-V
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IQFARNHPLMYNSVLPTG
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Similarity 29.0%;
27; Conservative 4
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  415
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                                                                                                                                -RTSSLKGYHMGLSNPRPGMCLPKK---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 368.5; DB 4
Pred. No. 1.6e-23;
9; Mismatches 167
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RESULT

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Best Local :
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Hu F.Q., Smith C.A., Pickup D.J.;
"Cowpox virus contains two copies
secreted form of the type II TNF r
Virology 204:343-356(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-83117629; PubMed-6961398;
Pickup D.J., Bastla D., Stone H.O., Joklik W.K.;
"Sequence of terminal regions of cowpox virus DN
repeated and unique sequence elements.";
Proc. Natl. Acad. Sci. U.S.A. 79:7112-7116(1982)
                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-BRIGHTON RED; Dietrich F.S., Ray C.A., Sharma A.D., Allen A., Pickup I Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases EMBL; AF482758; AAM13617.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Transcription of the terminal loop region of vaccinia virus initiated from the telomere sequences directing DNA resolution virology 181:716-720(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=BRIGHTON RED;
MEDLINE=91196263; Pu
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Darsons B.L., Pickup
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01-JUN-2002
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01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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STRAIN-BRIGHTON RED;
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    262
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                                                                                                                                                                                                                                                    VWVGGRGKVYHENFPEGKNASVRTVNIGSTKGSCQDKQDCGNYITLLERRGNGLLVCGTN
QLCRGDQGGESSLSVSKWNTFLKAMLVCS-DAATNRNFNRLQDVFLLPDPSGQWRDTRVY
                                              FDGPCGYDLYTADNVIPK-DGVRGAFVDKDGTY-DKVYILFTDTIGSKR---IVKIPYIA
                                                                     IRGES--ELYTSDTVMQNPQFIKATIVHQDQAYDDKIYYFFREDNPDKNPEAPLNVSRVA
                                                                                                                                 NGNPKCWKIDGSEDPKHRG--RGYAPYQKSKVTIISYNGC-VLSDINISKEG--IKRWRR
                                                                                                                                                                          ARKPSCWNLVNDSVVMSLGEMKGYAPFSPDENSLVLFEGDEVYSTIRKQEYNGKIPRFRR
                                                                                                                                                                                                                         LYTGVNGAVYTFSNNELNKTGLTNNNYITTSIKVEDKD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D.J.;
                                                                                                                                                                                                                                                                                                                                   Similarity
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(TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                    46488 MW;
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Pred. No. 4.
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                                                                                                                                                                                                                                                                                                              Mismatches
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AC Q8TD
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Matches 104
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
           Q8TDV7;
01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (JUN-2001) to the EMBL/GenBank/DDBJ EMBL; BC009113; AAH09113.1; -
InterPro; IPR003006; Iq_MHC.
InterPro; IPR001627; Sema.
Pfam; PF00047; 1g; 1.
Pfam; PF01403; Sema; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                           Q8TDV7
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Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                              S--DAATNRNFNRLQDVFLLPDDPSGQWRDTRVYGVFSNP--WNYSAVCVYSLGDIDRVF-
                                                                                                                                                                                                                                                                            DQAYDDKIYYFFREDNPDKNPE-APLNVSRVAQLCRGDQGGESSLSVSKWNTFLKAMLVC
                                                                                                                                                                                                                                                                                                                                NSLVLFEGDEVYSTIRKQEYNGKIPRFRRIRGESELYT - - - SDTVMQNPQFIKA-TIVHQ
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Similarity 34.1%;
04; Conservative 39
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                                                                                                                      302
                                                                                                                                              393
                                                                                                                                                                                                                                                                                                                                                                                                                                                       635 AA;
                                                           PRELIMINARY;
                                                                                                                                                                                          RTSSLKGYHMGLSNPRPGMCLPKK-----QPIPTETFQVADSHPEVAQR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       70694 MW;
            21,
21,
21,
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                     Last
           Last sequence update)
Last annotation updat
                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                      Score 354; DB 4; I
Pred. No. 2.4e-22;
9; Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       D994099B476B9210 CRC64;
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           update)
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RESULT
Q9C0C4
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Best Local Sin
Matches 126;
                                                                                                                                                                                                    Q9C0C4
Q9C0C4;
Q1-JUN-2001 (TrEMBLrel. 17,
Q1-JUN-2001 (TrEMBLrel. 17,
Q1-JUN-2002 (TrEMBLrel. 21,
          EMBL;
                                                The
                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                           KIAA1739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "semaphorin 3B (SEMA3B) cDNA."; Submitted (APR-2002) to the EMBL/GenBank/DDBJ EMBL; AB083186; BAB88870.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                               "Prediction of the coding sequences of unidentified The complete sequences of 100 new cDNA clones from
                                                                         MEDLINE=21082932; PubMed=11214970;
Nagase T., Kikuno R., Hattori A., Kondo Y.,
                                                                                                                                                                              KIAA1739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
InterPro;
                                      for
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                       Res
                      large proteins in vitro."; Res. 7:347-355(2000).
                                                                                                                                                                                                                                                                                                                    DFPDDVIQFARNHPLMYNSVLPTG
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                                                                                                                                                                                                                                                                                                                                            PIPTETFOVADSHPEVAQRVEPMG
                                                                                                                                                                                                                                                                                                                                                                    FQGSAVCVYSMNDVRRAFLGPFAHKEGPMHQWVSYQGRVPYPRPGMC-PSKTFGTFSSTK
                                                                                                                                                                                                                                                                                                                                                                                             WNYSAVCVYSLGDIDRVF-----RTSSLKGYHMGLSNPRPGMCLPKK-----Q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EPKFVKVFWIPESENPDDDKIYFFFRETAVEAAPALGRLSVSRVGQICRNDVGGQRSL-V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NPQFIKA-TIVHQDQAYDDKIYYFFREDNPDKNPE-APLNVSRVAQLCRGDQGGESSLSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GEMKGYAPFSPDENSLVLFEGDEVYSTIRKQEYNGKIPRFRRIRGESELYT---SDTVMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KDIGT-----ECMNFVKLLHAYNRTHLLACGTGAFHPTCAFVEVGHRAEEPVLRLDPGRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SQPEPHTVLFHEPGSFSVWVGGRGKVYHFNFPEGKNASVRTVNI------G
             AB051526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                        protein (Fragment)
IPR003599;
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          BAB21830.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83691 MW;
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Pred.
                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                        PRT;
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No. 4.1e-22;
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                                                              o Y., Okumura unidentified
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                                                                                                                                                                                                                   update)
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                                                brain which code
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RESULT
Q98VP6
ID VQ9
AC Q9
AC Q9
AC Q9
AC V9
AC V1
CO 
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Best Local :
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                                                                                                                                                                                                                                                                                Q98VP6;
01-JUN-2001
01-JUN-2001
01-OCT-2001
                    SEQUENCE FROM N.A.
STRAIN-BUFFALOPOX;
Gardner J.D., Tscharke D.C., Reading
"Evidence of a Pro-Inflammatory Role
A39R.";
                                                                                                                                                                                                                                            A39R.
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SMART; SM00410;
SMART; SM00423;
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                                                                                                                                                                                        Vaccinia virus.
Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
InterPro;
                                                                                                                                                                             Orthopoxvirus
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  Submitted (APR-2001)
                                                                                                                                                    NCBI_TaxID=10245;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NFVKKHPLMEEQVGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WNTFLKAMLVCSDAATNRNFNRLQDVFLLPDPSGQWRDTRVYGVFSNPWN---YSAVCVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VGSAYVPESVGSFTGDDDKVYFFFRERAVESDCYAEQVVARVARVCKGDMGGARTLQ-RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GKCPYDPAKGHAGLLVDGELYSA-TLNNFLGTEPIILRNMGPHHSMKTEYLAFWLNEPHF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IGSTKGSCQDKQDCGNYITLLE-RRGNGLLVCGTNARKPSCWNLVNDSVVMSLGEM---K
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127; Conserv
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IPR003659;
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l (TrEMBLrel.
l (TrEMBLrel.
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IG_1
PSI;
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25.7%;
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Pfam; PF00047; ig; 1.
Pfam; PF01403; Sema; 1.
SMART; SM00409; IG; 1.
SMART; SM00423; PSI; 1.
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Eukaryota; Metazoa; Chordata;
Eukaryota; Eutheria; Rodentia;
Mammalia; Eutheria; Rodentia;
MCBI_TaxID=10090;
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2002 (TrEMBLrel. 21,
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"A novel semaphorin, M-SemaK
sensory neurons.";
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Pred. No. 3.2e-21;
55; Mismatches 160;
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Pred. No. 7.
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Mismatches 126; Indels
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Best Local S
Matches 119
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Submitted (DEC-1999) to the
EMBL; AF217991; AAG17234.1;
FRONTING? Sema.
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Gu J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 50.4 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPRO01627; Sema.
Pfam; PF01403; Sema; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein. SEQUENCE 457 AA;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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J.R., Wan D.F., Zhao X.T.,
W.X., Huang Y., Qiu X.K.,
J., Han L.H.;
                                                                                                                                                                                                                                                               GRAAPSAPRARVLSLPARFGLPLRLRLLLVFWVAAASAQGHSRSGPRISAVWKGQDHVDF
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GEMKGYAPFSPDENSLVLFEGDEVYSTIRKQEYNGKIPRFRRIRGESELYT--
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Pred. No. 3.8e-20;
7; Mismatches 165;
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Qian L.F.,
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He L.P., Li
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H.N.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            boundary.";
boundary.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AB072930; BAB88691.1;
SEQUENCE 756 AA; 85196 MW; C36754C02541ED88 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; (
Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8QGU9;
01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEMA3F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Semaphorin 3F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Watanabe Y., Nakamura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Axon guidance of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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les 119; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SFSVWVGGRGKVYHFNFPEGKN-----ASVRTVN--IGSTKGSCQDKQDCGNYITLL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SS
                                                                  GPDGIETHFDELQDVFI-----QQTQDTKNPVIYAVFSASGSVFKGSAVCVYSMADIRMV
                                                                                                                                                                                      QPWNRTHLYVCGTGAYNPICAFINRGRKAQDYIFYLEPDKLESGKGKCSYDPKVDTVSAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLTLGWRAA-----HGKDGVPPTPRVQLSFKELKATGTAHF-FNFLLNSSDYRTLLKDED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLLVFWVAAASAQGHSRSG----PRISAVWK-----GQDHVDFS---QPEPHTVLFHEPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDGKGKSPYDPRHRAASVLVGEELYSGVAADLMGRDFTIFRSLGQRPSLRTEPHDSRWLN
                                                                                             INEELYAGV-YIDFMGTDAAIFRTMGKQTAMRTDQYNSRWLNDPAFVRAQLIPDSSERND
                                                                                                                                                                                                                                                                                                           EGDEVYSTIRKQEYNGKIPRFRRIRGESELYTSDTV----MQNPQFIKATIV-HQDQAYD
                                                                                                                                                                                                                                                                                                                                                                                                           ER-RGNGLLVCGTNARKPSC----WNLVNDSVVM----SLGEMKGYAPFSPDENSLVLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                        HDRMYVGSKDYVLSLDLHDINREPLIIHWPASQQRIEECILSGKNS----NGECGNFIRLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VCVYSMNDVRRAFLGPFAHKEGPMHQWVSYQGRVPYPRQA-CAPARPLAPSVPPRTSQTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NKWTTELKARLVCSVPGVEGDTHFDQLQDVFLL--SSRDHRTPLLYAVFSTSSSIFQGSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPKFVKVFWIPESENPDDDKIYFFFRETAVEAAPALGRLSVSRVGQICRNDVGGQRSL-V
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                        SSLKG-----YHMGLSNPRPGMC-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                   KSADAPLSPGVYSRIGRICLNDDGGHCCL-VNKWSTFLKARLVCSVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.1%; Score 320; DE 28.0%; Pred. No. 2.96 tive 64; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H.;
trochlear nerve by
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21,
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Last annotation update)
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                      LPKKQPIPTETFQVADSHPEVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156;
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                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9NS98 PRELIMINARY; PRT; 782 AA. Q9NS98; Q9H7Q3; Q1-OCT-2000 (TrEMBLrel. 15, Created) 01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Semaphorin sem2 (FLJ00014 protein).
                                                                                                                                                                                                                                                                                                SMART; SM00409;
SMART; SM00410;
SMART; SM00423;
                                                                                                                                                                                                                                                                                                                                                     InterPro;
InterPro;
                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                            Submitted (AUG-2000) to the EMBL/GenBank/DDBJ EMBL; AB029496; BAA98132.1; -- EMBL; AK024425; BABB15715.1; -- IPR003599; Ig.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Ohara O., Nagase T., Kikuno R., Okumura
"The nucleotide sequence of a long cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
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SEM2 OR FLJ00014)
                                                                                                                                                                                                                                                                                                                                Pfam;
                                                                                                                                                                                                                                                                                                                                          Ptam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 58-782 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted
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                                                                                                                                                                                                                                                                                                                                                                         InterPro;
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                                                                                                                                                                                                                                                      Local Similarity
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PF00047;
                                                                                             GEM---
                                                                                                                ECVR-----KGR-DPLTECANFVRVLQPHNRTHLLACGTGAFQPTC-----ALITV
                                                                                                                           ASVRTVNIGSTKGSCQDKQDCGNYITLLE-RRGNGLLVCGTNARKPSCWNLVNDSVVMSL
                                                                                                                                                           L-----RLDQAW-----PDPREVLWPPQPGQ---
                                                                                                                                                                           AQGHSRSGPRISAVWKGQDHVDFSQPEPHTVLF-HEPGSFSVWVGGRGKVYHFNFPEGKN 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HAVYP 416
                               PRPALRSDSDQSLLHDPRFVMAARIPENSDQDNDKVYFFFSETVP--SPDGGSNHVTVSR
                                                   ESELYTSD----TVMQNPQFIKATIVHQDQAYD-DKIYYFFREDNPDKNPEAPLN---VSR
                                                                        GHRGEHVLHLEPGSVESGRGRCPHEPSRPFASTFIDGELYTGL-TADFLGREAMIFRSGG
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                                                                                                                                                                                                                                                                                                                                                    IPR001627;
                                                                                                                                                                                                                                                                                                                                                              IPR003659;
                                                                                                                                                                                                                                                                                                                                                                         IPR003006;
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                                                                                                                                                                                                                                                                                     782 AA;
                                                                                                                                                                                                  -PSVPRLRLSYRDLLSANRSAIFLGPQGSLNLQAMYLDEYRDRLFLGGLDALYS
                                                                                                                                                                                                                                             Conservative
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Primates;
                                                                                                                                                                                                                                                                                     86700 MW;
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                                                                                         -KGYAPFSPDENSLVLFEGDEVYSTIRKQEYNGKIPRFRRIRG
                                                                                                                                                                                                                                           57; Mismatches 144;
                                                                                                                                                                                                                                                    Score 316.5; DB 4
Pred. No. 6.2e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata;
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                     85CB424874DF6663 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kozuma
                                                                                                                                                                                                                                                                                                                                                                                                                                                K.;
clone
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Homo.
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Q9H2E6;
Q1-E6;
Q1-MAR-2001 (TrEMBLrel. 1
01-MAR-2001 (TrEMBLrel. 1
01-JUN-2002 (TrEMBLrel. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

MEDLINE-20564339; PubMed-10993894;

MEDLINE-20564339; PubMed-10993894;
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InterPro;
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EMBL; AF279656; AAG29378.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00423; PSI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF01403; Sema;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The orthologous human and murine semaphorin 6A-1 proteins (SEMA6A-1/Sema6A-1) bind to the Enabled/Vasodilator-stimulated Phosphoprotein-like Protein (EVL) via a novel carboxyl-terminal Zyxin-like domain."; J. Biol. Chem. 275:39647-39653(2000).
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  KEQKSPDSTWTPVPDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAV
                                                                                                                                                                                                                                                                      YDDKIYYFFREDNPDKNPEAPLNVSRVAQLCRGDQGGESSLSVSKWNTFLKAMLVCS-DA
                                                                                                                                                                                                                                                                                                                               GKLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKW-----LKEPYFVQAV-----D
                                                                                                                                                                                                                                                                                                                                                                                     DEVYS---
                                                                                                                                                                                                                                                                                                                                                                                                                                     FIKVLLKKNDDALFVCGTNAFNPSCRNYKMDTLEPFGDEFSGMARCPYDAKHANVALFAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YI-TLLERRGNGLLVCGTNARKPSCWNLVNDSVVMSLGEMKGYA--PFSPDENSLVLFEG
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                                                         KGYHM - -
                                                                                                            DSHFYFNILQAVTDVIRING--RDV-VLATFSTPYNSIPGSAVCAYDMLDIASVF-TGRF
                                                                                                                                                                                                                     YGDYIYFFFREIAVEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPG
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IPR001627;
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114368 MW;
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Last annotation update)
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Pred. No. 5
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5.1e-18;
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RESULT Q9P2H9

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Search completed: March 14, 2003, 09:27:07 Job time: 26.8151 secs
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Nagase T., Kikuno R., Ishikawa K., Hirosawa M., Ohara O.;
"Prediction of the coding sequences of unidentified human genes.XVI.
The complete sequences of 150 new cDNA clones from brain which code
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KIAA1368.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       234 YDDKIYYFFREDNPDKNPEAPLNVSRVAQLCRGDQGGESSLSVSKWNTFLKAMLVCS-DA 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126 YI-TLLERRGNGLLVCGTNARKPSCWNLVNDSVVMSLGEMKGYA--PFSPDENSLVLFEG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 GKLYSATVTDFLAIDAVIYRSLGESPTLRTVKHDSKW-----LKEPYFVQAV-----D 229
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ISSUE=BRAIN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----SFSVWVGGRGKVYHFNFPEGKNASV-----RTVNIGSTKGSCODKODCGN 125
                                                                                                                                            KEQKSPDSTWTPVPDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFIKTHPLMDEAV 404
                                                                                                                                                                                                                 KGYHM ------GLSNPRPGMC-----LPKKQPIPTETFQVADSHPEVAQRV 389
                                                                                                                                                                                                                                                                                      DSHFYFNILQAVTDVIRING--RDV-VLATFSTPYNSIPGSAVCAYDMLDIASVF-TGRF 345
                                                                                                                                                                                                                                                                                                                                                       ATNRNFNRLQDVFLLPDPSGQWRDTRVYGVFSNPWNY---SAVCVYSLGDIDRVFRTSSL 349
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                                                                                                                                                                                                                                                                                                                                                                                                                               YGDYIYFFFREIAVEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVPG 289
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